OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: November 8, 2001, 08:03:35 ; Search time 5355.78 Seconds
                 (without alignments)
                 17816.367 Million cell updates/sec

Title: US-09-227-881-3
Perfect score: 6169
Sequence: 1 atcttgttcagttacctc..........cttgtgccccctccatgtcag 6169

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: gb_ba1:*
17: gb_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
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40: em_hum7:*
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42: em_om:*
43: em_or:*
44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
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50: em_sy:*
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55: gb_sts3:*
56: gb_sy:*
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64: gb_htg5:*
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73: gb_htg14:*
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78: gb_htg19:*
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82: gb_htg23:*
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84: gb_htg25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6105.4	99.0	79376	92	Z98750	Human DNA s
c 2	6054.4	98:1	170425	68	AC024490	Homo sap1
3	5300	85.9	5300	88	AF007562	Homo sap1
4	2677.4	43.4	2800	93	HSMYOC1	Homo sap1
5	1190.4	19.3	1228	85	AB006686	Homo sap1
6	1084.4	17.6	1086	93	AB006686S1	Homo sap1
7	651.2	10.6	1934	91	D88214	Homo sapien
8	640.4	10.4	1871	9	AX004457	Homo sapien AX004457 Sequence

```
RESULT 1
LOCUS       HS454G6     79376 bp    DNA             PRI    23-NOV-1999
HS454G6/c
DEFINITION  Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains
            trabecular meshwork inducible glucocorticoid response protein,
            TIGR, myocilin, ESTs and STS.
ACCESSION   Z98750
VERSION     Z98750.1  GI:2887277
KEYWORDS    1q24; myocilin; TIGR.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 79376)
  AUTHORS   Deadman,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-1997) Chromosome 1 Project Group
            (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquires:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Feb 14, 1998 this sequence version replaced gi:2465060.
            IMPORTANT: This sequence is not the entire insert of clone 454G6.
            It may be shorter because we only sequence overlapping sections
            once, or longer because we arrange for a small overlap between
            neighbouring submissions.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variations annotated may not be found in the sequence submission
            corresponding to the overlapping clone as we submit sequences with
            only a small overlap as described above.
            This sequence was generated from part of bacterial clone contigs of
            human chromosome 1, constructed by the Sanger Centre chromosome 1
            mapping group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1/
            This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            The true left end of clone 454G6 is at 1 in this sequence. The true
            left end of clone 56809 is at 79273.
            454G6 is from the library RPCI3 constructed at the Roswell Park
            Cancer Institute by the group of Pieter de Jong.
            For further details see http://bacpac.med.buffalo.edu/.
FEATURES             Location/Qualifiers
     source          1..79376
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1q24"
                     /clone="RP3-454G6"
                     /clone_lib="RPCI-3"
     repeat_region   435..472
                     /note="19 copies of 2 mer 82 % conserved"
     prim_transcript 1914..>3968
                     /note="match: multiple ESTs"
     repeat_region   4051..4183
                     /note="AluSq repeat: matches 1..133 of consensus
                     incomplete repeat"
     repeat_region   4200..4502
                     /note="AluSq repeat: matches 2..301 of consensus
                     incomplete repeat"
     repeat_region   4659..4851
                     /note="AluSx repeat: matches 2..194 of consensus
                     incomplete repeat"
     repeat_region   5216..5345
                     /note="AluJo repeat: matches 132..1 of consensus
                     incomplete repeat"
     repeat_region   7759..7907
                     /note="MIR repeat: matches 174..1 of consensus"
     repeat_region   7933..9328
                     /note="AluSp repeat: matches 1..289 of consensus"
     repeat_region   9332..9626
                     /note="TIGGER1 repeat: matches 1..1472 of consensus"
     repeat_region   10343..10642
                     /note="AluSp repeat: matches 1..300 of consensus"
     repeat_region   10643..10856
                     /note="TIGGER1 repeat: matches 2175..2417 of consensus"
     misc_feature    <10903..>16855
                     /note="endogenous retroviral sequence"
     repeat_region   10949..11384
                     /note="LTR2 repeat: matches 31..449 of consensus"
     repeat_region   15835..15870
                     /note="18 copies of 2 mer 83 % conserved"
     repeat_region   16856..17286
                     /note="LTR2 repeat: matches 31..449 of consensus"
     repeat_region   17287..17574
                     /note="LTR2 repeat: matches 1..449 of consensus"
     repeat_region   18294..18650
                     /note="AluSg repeat: matches 15..300 of consensus"
     repeat_region   18877..19180
                     /note="THE1B repeat: matches 358..1 of consensus"
```

ALIGNMENTS

No.	Score	P	Length	%	Accession	Description	Str
9	640.4	10.4	1871	9	AX004474	AX004474 Sequence	
10	640.4	10.4	1999	9	AR030962	AR030962 Sequence	
11	640.4	10.4	1999	9	AR066022	AR066022 Sequence	
12	640.4	10.4	1999	9	AR069089	AR069089 Sequence	
13	640.4	10.4	2000	9	U85257	U85257 Human trabe	
14	640.4	10.4	2002	9	A84847	A84847 Sequence 2	
15	635.6	10.3	2000	9	A84850	A84850 Sequence 2	
16	626.4	10.2	2061	93	HSAF001620	HSAF001620 Homo sapi	c
17	604.4	9.8	1512	9	AF001620	AF001620 Homo sapi	c
18	604.4	9.8	1512	9	A84848	A84848 Sequence 3	c
19	604.4	9.8	1512	9	AR030963	AR030963 Sequence	c
20	604.4	9.8	1512	9	AR066023	AR066023 Sequence	c
21	599.6	9.7	1512	9	AR069090	AR069090 Sequence	c
22	585.6	9.5	2800	94	A84851	A84851 Sequence 3	c
23	559	9.1	1016	94	MMUSMYOC1	MMUSMYOC1 Mus muscu	c
24	556.6	9.0	1969	9	AF041333	AF041333 Mus muscu	c
25	556.6	9.0	1969	10	MMTMIGP1	MMTMIGP1 Mus muscu	c
26	519.6	9.0	1969	10	AR020502	AR020502 Sequence 2	c
27	519.6	8.4	1491	9	I36470	I36470 Sequence 3	c
28	519.6	8.4	1491	10	I36471	I36471 Sequence 3	c
29	440.8	7.1	2004	94	AB013592	AB013592 Mus muscu	c
30	440.8	7.1	2059	94	AB039869	AB039869 Mus muscu	c
31	430.4	7.0	2044	94	AB019393	AB019393 Rattus no	c
32	426.2	6.9	2068	94	AF093567	AF093567 Rattus no	c
33	398.8	6.9	1473	7	AB027758	AB027758 Bos tauru	c
34	217	3.5	228	88	AF007564	AF007564 Homo sapi	c
35	189.8	3.1	161577	86	AC007688	AC007688 Homo sapi	c
36	189	3.1	214540	62	AC012404	AC012404 Homo sapi	c
37	189	3.1	161577	86	AC004973	AC004973 Homo sapi	c
38	187.8	3.0	97037	85	HUMWXD703	HUMWXD703 Homo sapien	c
39	187.8	3.0	135038	76	L78810	L78810 Homo sapien	c
40	187.6	3.0	193267	61	AC079767	AC079767 Homo sapi	c
41	187.6	3.0	139776	90	AC009409	AC009409 Homo sapi	c
42	187.4	3.0	139776	90	AL160165	AL160165 Human DNA	c
43	187.4	3.0	76727	92	HS821D11	HS821D11 Human DNA	c
44	185.8	3.0	151994	70	AL021453	AL021453 Human DNA	c
45	185.8	3.0	156958	69	AC026395	AC026395 Homo sapi	c
46	185.8	3.0	156958	69	AC025947	AC025947 Homo sapi	c
47	185.8	3.0	161499	63	AC015488	AC015488 Homo sapi	c
48	185.8	3.0	183216	79	AL161726	AL161726 Homo sapi	c

```
repeat_region    19767. .20013    /note="Aluy repeat: matches 301. .2 of consensus"
repeat_region    20051. .20118    /note="MLT2_internal repeat: matches 5002. .4750 of consensus"
repeat_region    20130. .20261    /note="MLT1F repeat: matches 539. .471 of consensus"
repeat_region    20264. .20722    /note="AluJb repeat: matches 131. .1 of consensus
                                   incomplete repeat"
repeat_region    20858. .21223    /note="MLT1F repeat: matches 482. .1 of consensus"
repeat_region    21216. .21302    /note="MLT2_internal repeat: matches 394. .1 of consensus"
repeat_region    21403. .21703    /note="MSTD repeat: matches 4520. .4433 of consensus"
repeat_region    21978. .22357    /note="MLT2_internal repeat: matches 3887. .3580 of consensus"
repeat_region    22363. .22524    /note="MLT2_internal repeat: matches 3218. .2839 of consensus"
repeat_region    22531. .22839    /note="MLT2_internal repeat: matches 2495. .2317 of consensus"
misc_feature     23286. .>23680   /note="STS G07544"
                 complement(23652. .24072)
misc_feature     24008. .24290    /note="STS G07436"
repeat_region    24408. .24290    /note="AluJo repeat: matches 298. .6 of consensus"
repeat_region    25895. .26364    /note="AluSx repeat: matches 302. .1 of consensus"
repeat_region    26397. .26697    /note="LTR2 repeat: matches 2. .449 of consensus"
repeat_region    26719. .27021    /note="AluSq repeat: matches 1. .302 of consensus"
repeat_region    26937. .29334    /note="AluSx repeat: matches 1. .302 of consensus"
repeat_region    29037. .30310    /note="AluSx repeat: matches 300. .3 of consensus"
repeat_region    30028. .30539    /note="AluSx repeat: matches 1. .301 of consensus"
repeat_region    30402. .30615    /note="MLT2B repeat: matches 264. .404 of consensus"
repeat_region    30402. >31136    /note="MLT2A repeat: matches 264. .453 of consensus"
prim_transcript  <30801.          /note="match: 5' EST AA256902 clone 682136"
repeat_region    30980. .31222    /note="MER4B repeat: matches 199. .431 of consensus"
repeat_region    31232. .31528    /note="AluSc repeat: matches 299. .1 of consensus"
repeat_region    31530. .31654    /note="MER4B repeat: matches 417. .540 of consensus"
repeat_region    31836. .32135    /note="AluY repeat: matches 300. .1 of consensus"
repeat_region    32200. .32301    /note="AluJo repeat: matches 186. .287 of consensus
                                   incomplete repeat"
repeat_region    32365. .32493    /note="MIR repeat: matches 206. .67 of consensus"
repeat_region    33283. .33399    /note="MIR repeat: matches 77. .196 of consensus"
repeat_region    33408. .33667    /note="AluY repeat: matches 1. .291 of consensus"
repeat_region    33956. .34043    /note="MIR repeat: matches 80. .167 of consensus"
repeat_region    34725. .34904    /note="AluJo repeat: matches 299. .127 of consensus
                                   incomplete repeat"

repeat_region    34907. .35207    /note="Aluy repeat: matches 300. .1 of consensus"
repeat_region    35212. .35344    /note="AluJb repeat: matches 133. .1 of consensus
                                   incomplete repeat"
repeat_region    36545. .36842    /note="AluJo repeat: matches 299. .1 of consensus"
repeat_region    38190. .38379    /note="MER3 repeat: matches 209. .13 of consensus"
repeat_region    38382. .38682    /note="AluSx repeat: matches 1. .302 of consensus"
repeat_region    38836. .38968    /note="MIR2 repeat: matches 145. .2 of consensus"
repeat_region    38983. .39279    /note="AluJb repeat: matches 354. .2 of consensus"
repeat_region    39418. .39773    /note="THEIA repeat: matches 3. .296 of consensus"
repeat_region    39775. .40120    /note="THE1B-INTERNAL repeat: matches 1580. .1234 of
                                   consensus"
repeat_region    40757. .41023    /note="AluJo repeat: matches 37. .301 of consensus
                                   incomplete repeat"
repeat_region    41307. .41589    /note="AluSq repeat: matches 21. .303 of consensus
```

Query Match
Best Local Similarity 99.0%; Score 6105.4; DB 92; Length 79376;
Matches 6165; Conservative 0; Mismatches 0; Indels 9; Gaps 5;

```
Qy      1 atctttgttcagtttacctcagggctattatgaaatgaaatgagaataaccaatgtgaaag  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68406 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 68347

Qy     61 tcctataaactgtatagcctccattcggatgtgtatgtcttgggatgatgataaagaatca 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68346 TCCTATAAACTGTATAGCCTCCATTCGGATGTGTATGTCTTGGGATGATGATAAAGAATCA 68287

Qy    121 ggaagaaggagtatccacgttagccaagtgtccgctcctatttagtga 180
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  68286 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCGCTCCTATTTAGTGA 68227

Qy    181 cagatgttgctcctgacagaagctatcctcaggaaactacatcacatccaatatggtaaatc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68226 CAGATGTTGCTCCTGACAGAAGCTATTCCTCAGGAAACATCACATCCAATATGGTAAATC 68167

Qy    241 catcaaacaggagctaagagaaacaggaatgtgagagtgggcacctgcccaaggaaaaatgccag 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68166 CATCAAACAGGAGCTAAGAAACAGGAATGTGGGCACTTGCCCAAGGAAAAATGCCAG 68107

Qy    301 gagagcaaatatgatgaaaaataaactttccctttgttttcaattccaaggaaaaatg 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68106 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAAGGAAAAATG 68047

Qy    361 atgaggaccaaaatcaatgaaataaggaaaaacagctcaaaaaagtgtttcaaatggg 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  68046 ATGAGGACCAAAATCAATGAAATAAGGAAAAACAGCTCAGAAAAAGTGTTTCAAATTCG 67987

Qy    421 taattaagtatttgttcctggaagagagacctccatgtgagcttgatgtgggaaaatgggaa 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67986 TAATTAAGTATTTGTTCCTGGAAGAGAGACCTCCATGTGAGCTTGATGTGGGAAAATGGGAA 67927

Qy    481 aaacgtcaaaagcatgatcgatccaaagtggattattatttaaaaccagat 540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  67926 AAACGTCAAAAGCATGATCTGATCCAAAGTGGCATTATTTATTTAAAAACCAGAT 67867

Qy    541 ggcatcactctggggaggcaagttcaggaaggacataacaataac 600
          ||||||||||||||||||||||||||||||||||||||||||
Db  67866 GGCATCACTCTGGGGAGGCAAGTTCATGGTTAGCAAAGGACATAACAATAAC 67807

Qy    601 agcaaaatcaaaattccgcaaatgcaggaggaaaatgggggactgggaaagcttccataac 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67806 AGCAAAATCAAAATTCCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 67747
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Qy    661 agtgattaggagcagttgacatgttcgcaacaccctccccgtctataccaggggaacacaaa 720
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67746 AGTGATTAGGCAGTTGACATGTTCGCAACACCTCCCCGTCTATACCAGGGGAACACAAAA 67687

Qy    721 attgactgggctaagcctggacttcaaggggaaatatgagagagacaaaacaaa 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67686 ATTGACTGGGCTAAGCCTGGACTTCAAGGGAAATATGAGAGAGACAAAACAAAA 67627

Qy    781 gacatggttaaaaggcaaccacagtaacatgtgagagcagtgagagcagca 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67626 GACATGGTTAAAAGGCAACCACAGTAACATTGTGAGCCCTCAGCA 67567

Qy    841 gggccctgaggggcattcgcctttagtaggtaggaggcaggaacctc 900
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  67566 GGGCCCCTGAGGGCATTTCGCTTTAGGAGGCAGCAGTGCCCCTCAGCA 67507

Qy    901 ttgaagatcatgaatcttaaccatctttaagtataaaacaaaatatcgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  67506 TTGAAGATCATGAATTTTAACCATTTTTAAGTATAAAACAAAATATGG 67447

Qy    961 tttagacatgggtcccaagtttcttaaggaaatctttaagagaaactc 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  67446 TTTAGACATGGGTCCCAAATTTTATAAAGTCAAGGAATAAATCTC 67387

Qy   1021 ggataggtcagaaatcattagaaatcactgttgtgtcccatccctaa 1080
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  67386 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACCCTAA 67327

Qy   1081 tgtcataagcagagatccacacacaagagggacccgatgtgtctca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  67326 TGTCATAGGCCTCACACCACAGGGCCCGATGTGTCTGACCTGGTA 67267

Qy   1141 gtgcctcaaccattgttaacgtgtcaatctcagtgtccaattcag 1200
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  67266 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTGTCCCAATTCTC 67207

Qy   1201 acctgagctcactgcaacctctgcctccaggtttcaagcaaatcctcccc 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  67206 ACCTGAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTCCTCCC 67147

Qy   1261 tacagccagagagctccgctgagggtgagggtctgtgtcttacactg 1320
          |||||||||||||||||||||||||||||||||||||||||||||||
Db  67146 TACAGCCAGAGAGCTCCGTGCAGGGTGAGGGTCTGTGTCTTACATCCTCTAC 67087

Qy   1321 cgcgtagctgggactacggcgcccggcgctaaatcttttgtattgttag 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  67086 ACCTGACCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTC 67027

Qy   1381 cgcgtagctgggactacggcgcccggcgctaaatcttttgtattgttag 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  67026 CGCGTAGCTGGGACTACAGGCGCCCGGCTAATTTTTGTATTTTTAGTAGGAT 66967

Qy   1441 gtttcaccatattagccggctggtcttgaacctcctgacctcaggtga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  66966 GTTTCACCATGTTAGCCAGGATGGTCTCGGGATCTCCTGACCTCGGTGA 66907

Qy   1501 agcctcctaaagtgctgggattacaggcgtgagccacc 1560
          |||||||||||||||||||||||||||||||||||||
Db  66906 AGCCTCCTAAAGTGCTGGGATTACAGGCCGTGAGCCACCGCGCCCAGCCT 66847

Qy   1561 ttaataaggaataactggactggtttactaaaccaacagacaaaagctgtga 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66846 TTAATAACGGAATAACTGGGACTAGGTTTACTAAACCAACAGACAAAAGCTGTGA 66787

Qy   1621 taatttcaggagttcttggatgtggggaatggtgccatggatcgcctagagac 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66786 TAATTTCAGGGAGTTCTTGGGATGTGGGGAATGGTGCCATTGGATCGCCTAGTCC 66727

Qy   1681 cactggtcctcatcacttccagtgctaagttaccacatttattt 1740
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Db  66726 CACTGGTCCTCATCACTTTCTCCCTCCATCCTCATTTTTCAGGCTAAGTTACCAGATTTTATT 66667
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Qy   1741 caccatgctgttttggtaagcctccaatcgttactgaaataagagtatactaaactag 1800
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Db  66666 CACCATGCTTTTTGTGGGTAAGCCTCCACATCCGTTACTGAAATAAGAGTATACATAAACTAG 66607

Qy   1801 ttccatttgggccatctcgtgtgtgttataggggggagggaggggcatacccccagagactcct 1860
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Db  66606 TTCCATTTGGGGCCCATCTCGTGTGTGTTATAGGGGGAGGGAGGGGCATACCCCCAGAGACTCCT 66547

Qy   1861 tgaagccccggcagagggtttcctctctgtgtgtggagccccgcaagcagcccctcagca 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66546 TGAAGCCCCGGCAGAGGGTTTCCTCTCAGTGTGGGGAGCCCCGCAAGCAGCCCCTCAGCA 66487

Qy   1921 tgggtgtcctgagcaacctccagccggttttccgtgttgttttgttatactctctagg 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66486 TGGGTGTCCTGAGCAACCTCCAGCCGGTTTCCGTGTTGTTTTGTTATACTCTCTAGG 66427

Qy   1981 gacctgttgtcttcattctgtgtggactccgttcattcatcatcattgacaatt 2040
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Db  66426 GACCCGTTGTCTTCATTTCTGTTGGACTCGTTCATTCATCATTGACAATT 66367

Qy   2041 tattgagtactttatatctgccagacaccagacaaaatggtgagcagtcactgc 2100
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Db  66366 TATTGAGTACTTATATTCTGCCAGACACCAGACAAAATGGTGAGCAGTCACTGC 66307

Qy   2101 cctacccttcgtgtgaggtgacagtttctctcagtgctccctaggcgcccctcc 2160
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Qy   2161 gccaacttaaacccagtgctgctgaaaggaaaatctcgttctcgttcatttgaccaggt 2220
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Qy   2221 agcatcccttaacacaaggccaactcctccccagccctagccccctcc 2280
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Db  66186 AGCATCCCTTAACACAAGGCCAACTCCTCCCCAGCCCTAGCCCCCTCC 66127

Qy   2281 cctacttcgttgagagtcttcaaggcctcccatccagct 2340
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Db  66126 CCTACTTCGTTGAGAGTCTTCAAGGCCTCCATCCAGCTGGGCCT 66067

Qy   2341 tgggacagctgggggtgagcgggtgctgaaatcgtgaaatggcaggct 2400
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Qy   2401 ccagaaaggaaatggagagggaaacatagtctaacggaagactgagttttc 2460
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Qy   2461 ctcagaaggggaaagggcctccagtccaagtccagttttcatgaagggagttggggg 2520
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Qy   2521 tggggacgctggggcgtgggggtgctgaaaggaaggcaaggtgaaagctgaa 2580
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Qy   2581 gctgcccagagatgttcagtgttcacgggctggagagttttccggttcctgtgagc 2640
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Db  65826 GCTGCCCAGAGTGTTCAGTGTTCACGGGCTGGAGAGTTTTCCGTTGCTTCCGTGAGC 65767

Qy   2641 ctttttattctttctcctctctgggggaaaggagaaagtctattttccatggagtcc 2700
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Db  65766 CTTTTTATCTTTTCCTCGTTGGGGGAAAGGGAGAAGTCTATTTTCATGAAGGGAGAGTTTC 65707

Qy   2701 ataaagtcagctgttaaaattccaggtgtgcatggtgtttctctcacgaatggccttat 2760
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Db  65706 ATAAAGTCAGCTGTTAAAATTCCAGGTGTGCATGGGTTTTTCTCACGGGTCATGGGCCTTTAT 65647

Qy   2761 ttaatgggaatataggaagagagcagagagcagttggagagccgttaatcacggaagaagtgac 2820
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Db  65646 TTAATGGGAATATAGGAAGAGAGCAGAGAGTCATTTTCCTTAACGGAAGAAGTGAC 65587

Qy   2821 tgggagtgtcttcttcagtctctgggcaactactcagccctgtggtggactggcttta 2880
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Db   65586 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 65527

Qy    2881 tgcaagacggtcgaaaaccttggaatcaggagactcggttttctttctggttctgccatt 2940
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Qy    2941 ggttggctgtgcgaccgtgggcaagtgtctctccttccctgggccatagtcttctctgct 3000
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Db   65466 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 65407

Qy    3001 ataaagacccttgcagctctcgtgttctgtgaacacttccctgtgattctctgtgagggg 3060
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Qy    3061 ggatgttgagaggggaaggaggcagagctggagcagctgagccacaggggaggtggaggg 3120
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Qy    3121 ggacaggaaggcaggcagaagctgggtgctccatcagtcctcactgatcacgtcagactc 3180
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Qy    3181 caggaccgagagccacaatgcttcaggaaagctcaatgaacccaacagccacatttcct 3240
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Qy    3241 tccctaagcatagacaatggcatttgccaataaccaaaaagaatgcagagactaactggt 3300
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Db   65166 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 65107

Qy    3301 ggtagcttttgcctggcattcaaaaactgggccagagcaagtggaaaatgccagagattg 3360
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Qy    3361 ttaaacttttcaccctgaccagcaccccacgcagctcagcagtgactgctgacagcacgg 3420
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Db   65046 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 64987

Qy    3421 agtgacctgcagcgcaggggaggagaagaaaaagagagggatagtgtatgagcaagaaag 3480
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Qy    3481 acagattcattcaagggcagtgggaattgaccacagggattatagtccacgtgatcctgg 3540
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Qy    3781 taaagccaaacagattcaagcctaggtcttgctgactatatgattggtttttgaaaaat 3840
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Db   64506 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 64447

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Db   64446 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 64388

Qy    4020 cagtttggaaatatttacttcacaagtattgacactgttgttggtattaacaacataaag 4079
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Qy    4200 gggattattaacctacagtccagaaagcctgtgaatttgaatgaggaaaaaattacattt 4259
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Db   64147 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTATTCCATTGCGAATAGAGCCATAA 64088

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Db   63847 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 63788

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RESULT 2

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Qy      6115 cctgaagagcttcattagattagttgggttcaagagttcttggtgccctcccatgtcag 6169
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*  arbitrary. Gaps between the contigs are represented as
*  runs of N, but the exact sizes of the gaps are unknown.
*  This record will be updated with the finished sequence
*  as soon as it is available and the accession number will
*  be preserved.
*
*        1    1300: contig of 1300 bp in length
*     1301    1400: gap of 100 bp
*     1401    2412: contig of 1012 bp in length
*     2413    2512: gap of 100 bp
*     2513    4147: contig of 1635 bp in length
*     4148    4247: gap of 100 bp
*     4248    5455: contig of 1208 bp in length
*     5456    5555: gap of 100 bp
*     5556    6997: contig of 1442 bp in length
*     6998    7097: gap of 100 bp
*     7098    8534: contig of 1437 bp in length
*     8535    8634: gap of 100 bp
*     8635   10164: contig of 1530 bp in length
*    10165   10264: gap of 100 bp
*    10265   10487: contig of 223 bp in length
*    10488   10587: gap of 100 bp
*    10588   12420: contig of 1833 bp in length
*    12421   12520: gap of 100 bp
*    12521   14843: contig of 2323 bp in length
*    14844   14943: gap of 100 bp
*    14944   17265: contig of 2322 bp in length
*    17266   17365: gap of 100 bp
*    17366   20071: contig of 2706 bp in length
*    20072   20171: gap of 100 bp
*    20172   23531: contig of 3360 bp in length
*    23532   23631: gap of 100 bp
*    23632   26137: contig of 2506 bp in length
*    26138   26237: gap of 100 bp
*    26238   29858: contig of 3621 bp in length
*    29859   29958: gap of 100 bp
*    29959   36225: contig of 6267 bp in length
*    36226   36325: gap of 100 bp
*    36326   44015: contig of 7690 bp in length
*    44016   44115: gap of 100 bp
*    44116   49493: contig of 5378 bp in length
*    49494   49593: gap of 100 bp
*    49594   56796: contig of 7203 bp in length
*    56797   56896: gap of 100 bp
*    56897   62860: contig of 5964 bp in length
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*    72653   83310: contig of 10658 bp in length
*    83311   83410: gap of 100 bp
*    83411   92992: contig of 9582 bp in length
*    92993   93092: gap of 100 bp
*    93093  103886: contig of 10794 bp in length
*   103887  103986: gap of 100 bp
*   103987  119418: contig of 15432 bp in length
*   119419  119518: gap of 100 bp
*   119519  136695: contig of 17177 bp in length
*   136696  136795: gap of 100 bp
*   136796  153977: contig of 17182 bp in length
*   153978  154077: gap of 100 bp
*   154078  170425: contig of 16348 bp in length.

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ORIGIN

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Qy    3776 aagagtaaagcaaacagatccaaacctagggtcttgctgactgatatgatgggtttttgta 3835
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Db   67465 AAGAGTAAAGCAAACAGATTCAAAGCTAGGGTCTTGCTGACTATGATGGTTTTTGA 67524

Qy    3836 caggcaagttggaaatatcttacctcaacagtatgacagtgttgttggttattaacaaca 3895
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Qy    3896 agctgtaaaacaacacccagttgtaaatgtctcaagttcaggcttaactctgacagttg 3955
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Qy    3956 caaa-aagaataagaatctttagagcaaactgtgttctcccacatctagaatcaca 4014
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Qy    4015 caggcagttggaaatatattcactgacagtgttgttggttattaacaacaacca 4074
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Qy    4075 taaagttgctcaaaggcaatcaatcatttatttcattccaattgggaatagagc 4134
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Qy    4135 gtatattttattggccatttgcttttgtttattttattaatgta 4194
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Qy    4195 aagcaggggatattattaacctacagtccagagaaaccctgtgaatttgaatgagggaaaaaaatta 4254
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Qy    4255 cattttctggttttttaccacctccaactaaaatttacattccaattggccgaatagagc 4314
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Db   67944 CATTTTGTTGTTTTTAACACCTTCTAACTAAAATTTAATTCCGAATGGCCAAT 68003

Qy    4315 cataaactcaaagtggtaataacaaacctgtcaataacatagaaatcaca 4374
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Qy    4375 gacatttttacttatattacagttgtcggatacgttgtaagtgaaatattatactca 4434
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Qy    4435 aaactaacttgaaattagaactcccctggctggatctctgttttaaacatattaataaacatg 4494
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Qy    4495 tttaaaatttgatattcattatcatcattgttccttgtaatcta 4554
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Db  68184 TTTAAAATTTGATATTTGATAATCATTATATTTCATTATTTGTTTCCTTTGTAATTCTA 68243

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Db  68244 TATTTTATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCAGATTTCACCAAATGAGT 68303

Qy   4615 tcttggcatgcacacacacagagtaagaactgatttagagaggtacacattggtgc 4674
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Qy   4855 ttgtttggatctccagttctcagcacatagtgcctggcggttctcaatgagttt 4914
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Qy   5035 gagatataggagaactattattgggtatgggggtcgcaataaaattgggagtgttcttttc 5094
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Qy   5095 aaactccaaacagctctggaagggttattttctaagaaatcttgctggcacgtgaaggc 5154
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Qy   5155 aacccccctgtcacagccccagcgccccaggtaacctcagag 5214
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Db  68842 AACCCCCTGTCACAGCCCCAGCCTCACGTGGCCACCTCGTCTTCCCCCCATGAA 68901

Qy   5215 ggctggctgggcagtagtatatataaaacctctctcggaagaccaaggcca 5274
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Qy   5275 cccatccaaggcacctcctcagccacagcagagggtccagcaagcctctg 5334
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Qy   5335 caatgagggttcctcctgtgcacgttcgctgtccatccaatgtgtccagc 5394
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Qy   5395 tgctgcttctggcctggtgggatgtgggggccaggacacagctcaaggaag 5454
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Qy   5455 ccaatgaccaagagtggccagatgccagtataccttcagtgtggtccagtc 5514
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Qy   5515 gctgtcccaagcgagcaggccaggtggggccatgccactgatccaatgaatcca 5574
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Qy   5575 cccaaacgcttagacctgggaggccacaaagctcggcctcccc 5634
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Db  69262 CCCAACGCTTAGACCTTGGAGGCCACCAAAAGCTCGACTCAGCTCCTGGAGGCCTCC 69321
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Qy   5635 accaattgacctggaccaggctgccaggccccaggaggacccaggaggggctgcagagg 5694
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Db  69322 ACCAATTGACCTTGGACCAGGCTGCCAGGCCCCAGGAGGACCCAGGAGGGGCTGCAGAGG 69381

Qy   5695 agctgggcaccctgaggcggggagcgggggaccagctggaaacccaaaccagagagttggaga 5754
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Qy   5755 ctgcctacagcaacctcctccgagagacaagtcagttctggagaggaagagaagacgagctaa 5814
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Qy   5815 ggcaagaaaatgagaaatctggccaggcgcagtggctcctcacggagagtcag 5874
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Qy   5875 tgaggaaggggccagtgtcccagtgggggaccctgagagtctcggggctgtggc 5934
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Qy   5935 gagaaggtaagaatgcagagtgtgggggactctgagttcaggttggtgatatggctagt 5994
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Db  69622 GAGAAGGTAAGAATGCAGAGTGTGGGGGACTCTGAGTTCAGGAGGTCGATATGGCCTGTAGT 69681

Qy   5995 gacctgctacaggcgccagggcctc------cctgcccttctcctagacactgcacagct 6050
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Qy   6051 agcacaagacagatgaattaaggaaaagcaca-cgatcacctcaagtattactagtaatt 6109
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Db  69742 AGCACAAGACAGATGAATTAAGGAAAAGCACACCACCTTCACGTTATTACTTAGTAATT 69801

Qy   6110 tagctcctgagagcttcatttagattagtggttcaagagttcttgtgccctccaatgtcag 6169
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Db  69802 TAGCTCCTGAGAGCTTCATTTAGATTAGTGGTTCAAGAGTTCTTGTGCCCTCCAATGTCAG 69861
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BASE COUNT   1483 a   1152 c   1236 g   1429 t

ORIGIN

/note="additional 3' sequence deposited as TIGR mRNA with
GenBank Accession Number U85257"
/product="trabecular meshwork inducible glucocorticoid
response protein"

Query Match   85.9%;   Score 5300;   DB 88;   Length 5300;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 5300;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy        1 atctttgttcagttacctccaggtgctattatgtgaaatgagataaccaatgtgaaag      60
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Db        1 ATCTTTGTTCAGTTTACCTCCAGGTGCTATTATGTGAAATGAGATAACCAATGTGAAAG      60

Qy       61 tcctataaactgtatagcctccattcggatgtatgtcttgttgggcaggatgataagaatca     120
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Db       61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTGTTGGGCAGGATGATAAAGAATCA     120

Qy      121 ggaagaaggagtatcccaacgttagtccaggtcgtgtctgctcttattagtga     180
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Db      121 GGAAGAAGGAGTATCCCACGTTAGTCCAGGTCGTCGTCCTCTTATTTAGTGA     180

Qy      181 cagatgttgctcctgacagaagctgtattcttctcaggaaaatcaataaatatggtaaatc     240
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Db      181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCTCAGGAAAATCAATAATATGGTAAAATC     240

Qy      241 catcaaaacaggagctaagaaacaggagtgagagtgagaaatgccag     300
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Db      241 CATCAAAACAGGAGCTAAGAAACAGGAGTGAGAATGGGCACTTGCCCAAGGAAAAATGCCAG     300

Qy      301 gaggagctcaaagctgatctgaatcccacttgtttttaattcaggaaaaccagat     360
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Db      301 GAGGAGCAAAATAATGATGAAAAACTTTTCCCTTTGTTTTTAATTCAGGAAAAATG     360

Qy      361 atgagggaccaaaatcaatgaataaggaaaaacagctcagaaacagtgtttccaaattgg     420
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Db      361 ATGAGGACCAAAATCAATGAATAAGGAAAAACAGCTCAGAAAAAGAGATGTTTCCAAATTGG     420

Qy      421 taattaagtattgttgttcccttgggaagaagaacctccatgtgaagcttgatgggaaaatgggaa     480
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Db      421 TAATTAAGTATTTGTTCCTTGGGAAGAGAGAACCTCCATGTTAGCAAAGGACTAACAATAAC     480

Qy      481 aaacgtcaaagcatgatctgatcagaatcccaaagtggattattattttaaaacccagat     540
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Db      481 AAACGTCAAAAGCATGATCTGATCAGAATCCCAAAGTGGATTATTATTTTAAAACCAGAT     540

Qy      541 ggcatcactctgggaggagtcaggaaagtcatgttagcaaggacataacaaataac     600
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Db      541 GGCATCACTCTGGGAGGAGGTCAGGAAAGTCATGTTAGCAAAGGACATAACAATAAC     600

Qy      601 agcaaaatcaaaattccgcaaaatgcaggaggaggactgggaaaagcttcatgaac     660
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Db      601 AGCAAAATCAAAATTCCGCAAAATGCAGGAGGAGGACTGGGAAAAGCTTCATAAC     660

Qy      661 agtgattaggctgaccatgttcgcaacaccacccccgctctaccaggggaacacacaaa     720
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Db      661 AGTGATTAGGCTGACCAGTTGTCGCAACAGTTCTCTCTATACCAGGGAACACCACAAA     720

Qy      721 atgactgggctaagcctggactttcaagggaaatatgagagacaaacaaaa     780
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Db      721 ATTGCACTGGGCTAAGCCCTGGACTTTCAAGGGAAATATGAGAGACCAAACAAAA     780

Qy      781 gacatggttaaaggcaacacagaacaatctgtgacctcaaaagcagcaagtgccctccagca     840
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Db      781 GACATGGTTAAAAGGCAACCAGAACATTGTGACCTCAAAAGCAGCAGTGCCCCTCAGCA     840

Qy      841 gggaagccctgaggcgcattgcctttaaggaaggccaagtttttcttaaggaagaaactc     900
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Db      841 GGGACCCTCAGGCATTTGCCTTTAAGGAAGGCCAAGTTTGCCTTTAAGGAATCTTAAGAAACTC     900

Qy      901 ttgaaagatcatgaatttaaccatttaagtataaaaaacaaatatcgcgatgcataatcag     960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      901 TTGAAAGATCATGAATTTAACCATTTAAGTATAAAAAACAAATATGCGATGCATAATCAG     960

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Db      961 GGATAGGTCAGAAATCAATTAGAAAATCAACTTGTTGTCCCAATCCTAACCTTTTCAGAATGATC    1020

Qy     1021 tttagacatgggtcccaatttataaagtcaaggcatcacaaggatcaacgtgtcccagctcc    1080
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Db     1081 TGTGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACACCCCAA    1140

Qy     1141 gtgcctcaaccacttgttaacgtgtcatctcagtagggtcccattacaaatgccactccccc    1200
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Db     1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGGTCCCATTACAAATGCCACTCCCC    1200

Qy     1201 tgtgcagcccatccccgtcacaggagaagtctcccaactctagaactctgaatcacgatgt    1260
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Qy     1261 tacagccaagaagctccgtgaggtgtggggtctgtgtcttagacacctgatcgatctctac    1320
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Qy     1321 acctgagctcactgcaaacctctgcctcccccaggttcaagcaatcttccctgtctctcagcc    1380
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Qy     1441 gtttcaccatattacaggctggtctcggatctcctgacctcgtgatcccacccacctc    1500
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Qy     1501 agccttccctaaagtgctgtgggattacaggcgtgagtcaccgcgcccggccaaggtcagtgt    1560
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Qy     1561 ttaataaggaataaacttgaaatgggtttactaaacacacacaggaaaactgtga    1620
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Qy     1681 cactggtccctcactctttcttcaggtggctaagttaccattttatt    1740
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Db     1681 CACTGGTCCCTCACTCACTTTCTTCCCTCATTTTCAGGCTAAGTTACCATTTTATT    1740

Qy     1741 caccatgcttttctggtttactgaacatcgttactgaaatataacataacctag    1800
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Db     1741 CACCATGCTTTTCTGGTTTAAGCCTCCAACCTTACTGGAATATACATAAACTAG    1800

Qy     1801 ttccaattggggcccactgttgtgtgtataaggagggagggagggagactcct    1860
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Qy     1861 tgaagccccgcagaggttcctctccagctgtggggagcgcgagcaagcgcgggggtcc    1920
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Qy     1921 tgggtgtcctgagcaacctgccactggttgtttgtgttatcatctctcagg    1980
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Db  1981 GACCTGTTGCTTTCTTATTTCTGTCTGACTCGTCTTCATTCAGGCCATTCATTGACAATT 2040

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Qy  2101 cctacccttcgtggagttgacagtttcctcaatggaagacgtgccagagagaaattaatagcca 2160
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Qy  2161 gccaacttaaacccagtgctgaaagaaagagaat aaaacccatctttgaagaattgtgcgc 2220
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Qy  2521 tggggacagctgagcgggtgctggaaagtgtgaaaagggcaaggctgaa 2580
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Db  2521 TGGGGACAGGCTGGGCTGAGCGGGTGCTGAAAAGGGCAAGGCTGAA 2580

Qy  2581 gctgcccagatgttcagtgttcctgctccctgtgagc 2640
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Qy  2641 ttaatgggaatatagaggcagctcattttcctggagggccgttaaattcacgggaagaagtgac 2700
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Qy  2701 ataaagtcagctgttaaaattccagggtgtgcatgggtttcttccttcacgaaggcccttat 2760
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Qy  2821 tggagtctcttttcatgtcttctcgggcaactactcagctcagcaagcccctgtggtgacttggctta 2880
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Qy  3601 cctgattctcctaatactataattttccttacaagctgagtaattctgagcaagtcacaag 3660
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Db  3601 CCTGATTTCTTAATACTAATATATTTTTCCTTTACAGCCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy  3661 gtagtaactgaggggctgtaagaattcactaacttagttctcctttattaagttccaccctggttatcgatctcttctggatctg 3720
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Qy  3721 ggagttagcagcacaagggcaatcccgtttctttaacaggagaggaaaacattcctaagag 3780
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Db  5281 CAGGCACCTCTCAGCACAGC 5300
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RESULT   4

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LOCUS       HSMYOC1       2800 bp    DNA             PRI       21-APR-1998
DEFINITION  Homo sapiens myocilin (GLC1A) gene, promoter and exon 1.
ACCESSION   AF049791
VERSION     AF049791.1  GI:3065670
KEYWORDS    .
SEGMENT     1 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Characterization and comparison of the human and mouse GLC1A
            glaucoma genes
  JOURNAL   Genome Res. (1998) In press
REFERENCE   2  (bases 1 to 2800)
  AUTHORS   Fingert,J.H., Ying,L., Swiderski,R.E., Nystuen,A.M., Arbour,N.C.,
            Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
            Hawkins Drive, Iowa City, IA 52242, USA
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     exon            1906..2509
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BASE COUNT      781 a    588 c    673 g    758 t
ORIGIN
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Query Match           43.48;  Score 2677.4;  DB 93;  Length 2800;
Best Local Similarity  99.78;  Pred. No. 0;  Indels 8;  Gaps 5;
Matches 2736;  Conservative 0;  Mismatches 1;
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Db     1 AGCGCAGGGGAGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGACCAAGAAGACAGATTCAT 59

Qy  3491 tcaaagggcagtgggaattgaccacacaggagttatatgtccacgtgatcctgggttctaggag 3550
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Qy  3551 gcagggctatattgtggggggaaaaatcaagttcaagggggagtcgggagaacctgatttct 3610
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Db   120 GCAGGGCTATATTGTGGGGGGAAAAATCAGTTCAAGGGGAGTCGGGAGACCTGATTTCT 179

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Db   420  ATGTTTACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA  479

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Db   480  CCCAGTTGTAAAATGTCTCAAGTTCAGCGCTTAACTGCAGAACCAAATCAAATAAGAAATAGAA  539

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Qy  4090  gcaatcattatttcaagttactctctgacacgttttgtatattatttatttggct  4149
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Db   719  ATTGCCATTTGCTTTTGTCTTTTTTCTCTTTGGGTTTATTTTAATGTAAAAGCAGGGATATTA  778

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Db   779  ACCTACAGTCCAGAAAGCCTGTCGAATTTGAATTTGAATCAGAGGAAAAAATTATACTTTGTTTTTTAC  838

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Db   839  CACCTTCTAACTAAAATTTACATTTTATTTCATTGGGAATAGAGCCCATAAACTCAAAGTG  898

Qy  4330  gtaataacagtacctgtgatttctgtcattaccaatagaaatccacagacaatttatacat  4389
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Db   899  GTAATAACAGTACCTGTGATTTGTTCATTACCAAATAGAAATCACACAGACAATTTTATACTTAT  958

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Qy  4750  atctggcgctctatagggagtgctctcccaggcctggtagggtgctgcctgtcctttgtttcgttc  4809
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Db  1319  ATCTGCCGGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTGCTGTGTCTTGTTTC  1378

Qy  4810  tggctggctgttattttttcctctgtccctgctacgtcttaaaggacttgttgttgatctcca  4869
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Db  1379  TGGCTGGCTGTTATTTTTTTCTGTGTCCCTGCTACGTCTTAAAGGACTTGTTGTTTGGATCTCCA  1438

Qy  4870  gttcctagcatagtgcctggacagtgcaggtgttcaatgaagtttgcagagaagtgaatggaa  4929
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Db  1439  GTTCCTAGCATAGTGCCTGGACACAGTGCCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA  1498
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Db  1499  ATATAAACTAGAAATATTATCCTTTGTTGAAATCAGCACACCAGTAGTCTCGTGGTAAGTGT  1558

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Qy  5050  ttattgggtatgggtgcataaatttgggagtttcctttttaaaaagaaaacagaa  5109
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Db  1619  TTATTGGGGTATGGGTGCATAAATTTGGGATGTTCTTTTTAAAAAGAAAACAGAC  1678

Qy  5110  ttctggaaggttattttcttaaagaatcttgctgtggcagtgcaatcccccctgtgcac  5169
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Db  1679  TTCTGGAAGGTTATTTTCTTAAGAATCTTGCTGGGCAGTGCAATCCCCCCCGTGCAC  1738

Qy  5170  agccccacccagcctcacgttttctgacagttctaacatataatttatttatt  5229
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Db  1739  AGCCCCACCCCAGCCTCAGGTGGCCACCTCTGTTCTCCCCATGAAGGGCTCCCCAG  1798

Qy  5230  tatatataaacctctctgggagtcgggggatcgggggccagcaaggtcaaatgacccacct  5289
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Db  1859  CTCAGCACAGCAGAGCTTTCCAGAGGAAGCCCTCACCAGCCTGCAATGACGGAGTTCTTTCT  1918

Qy  5350  gtgcacgttgctgcagctttgggcctgagatgccaagtcctgtgctctgctcctggcct  5409
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Db  1919  GTGCACGTTGCTGCAGCTTTGGGCCTGAGATGCCAGTCCTGTGCTCCACTGCTCTGTGGCT  1978

Qy  5410  gcctggtgttggggatgtggggccagcagagacagctcaaggagggaaggccagcaagagtg  5469
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Db  1979  GCCTGGTGTGGGGGATGTGGGGCCAGGACAGCTCAGGTCACCAAGCTCAGGCACCT  2038

Qy  5470  gccggatcgcagtataccttcaagtgtgtggggccagcacccagagcaga  5529
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Db  2039  GCCGGATGCCAGTATACCTTCAGTGTGTGGGCCGCAGAGCCCTGCCAGCAGAGA  2098

Qy  5530  gccaggccaatgtcagtcatccataacttacagagacagctacagcgccttagacc  5589
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Db  2099  GCCAGGCCATGTCAGTCATCCATAACTTACAGAGACAGCAGCGCTTACAGACC  2158

Qy  5590  tggaggcaccaaggccaaagtcgactcaagctccctgggagagaagcaatgacctgg  5649
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Db  2159  TGGAGGCCACCAAGGCCAAAGTCGACTCAGCTCCCCTGGGAGAGAAGCGACCTTGG  2218

Qy  5650  accaggctgcacaggccagggagaggaggagaagagctgagagggagtcccagca  5709
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Db  2219  ACCAGGCTGCCAGGCAGGGAGAGGAGGAGAAGAGCTGAGAGGGAGTGGGCACCCTGA  2278

Qy  5710  gggcgggagggagcgggaccagctggaaacccaaacacagagagtggagactgcctcagcaacc  5769
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Qy  5770  tcctccgagacaagtcagttctggaggaagagaagcgaagcaataaaaatgaga  5829
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Db  2339  TCCTCCGAGACAAGTCAGTTCTCGGAGGAAGAGAAGCGAGACTAAGGCAAAATGAGA  2398

Qy  5830  atctggcaggagggttcggaaagcagtcaagaggtagcagaagagggggccagt  5889
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Qy  5890  gtccccagacccgagacaactgctccggggctgctgccaccaagagaaaggtaagaatg  5949
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Qy  5950  cagagtgggggactctgagttcagcaggtgatatgggtcgtaagtgacctgctacagg  6009
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Db  2519  CAGAGTGGGGGGACTCTGAGTTCAGCAGGTGATGATATGGCTCAGAGTTGACCTGCTACAGGCG  2578
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Qy  6010 ctccaggcctc-----cctgacccttctcctaggagaactgcacagctacacagagacagatg 6065
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Db  2579 CTCCAGGCCTCCCTGCCTCCCCTTTCTCCCTTAGAGACTGCACAGCTAGCACAGAGACAGATG 2638

Qy  6066 aattaaggaaagcaca-cgatcaccttcaagtattactagttagctcctagaagct 6124
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Db  2639 AATTAAGGAAAGCACACGATCACCTTCAAGTATTACTAGTTAGCTCCTGAGAGCT 2698

Qy  6125 tcattttagattagttggttcaagttcttgtgtgccctccatgtcag 6169
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Db  2699 TCATTTAGATTAGTTGGTTCAAGTTCTTGTGTGCCCTCCATGTCAG 2743
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RESULT 5

AB00668681

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LOCUS       AB00668681      1228 bp    DNA          PRI    14-APR-2000
DEFINITION  Homo sapiens gene for myocilin, exon 1, complete sequence.
ACCESSION   AB006686
VERSION     AB006686.1  GI:2828342
KEYWORDS    myocilin.
SEGMENT     1 of 3
SOURCE      Homo sapiens
            clone:KB780C12.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Escribano,J., Ortego,J. and Coca-Prados,M.
  TITLE     Isolation and characterization of cell-specific cDNA clones from a
            subtractive library of the ocular ciliary body of a single normal
            human donor: transcription and synthesis of plasma proteins
  JOURNAL   J. Biochem. 118 (5), 921-931 (1995)
  MEDLINE   9631803
REFERENCE   2  (sites)
  AUTHORS   Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.,
            Sunden,S.L., Nishimura,D., Clark,A.F., Nystuen,A., Nichols,B.E.,
            Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.
  TITLE     Identification of a gene that causes primary open angle glaucoma
  JOURNAL   Science 275 (5300), 668-670 (1997)
  MEDLINE   9115493
REFERENCE   3  (sites)
  AUTHORS   Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
            Mashima,Y., Oguchi,Y. and Shimizu,N.
  TITLE     A novel myosin-like protein (myocilin) expressed in the connecting
            cilium of the photoreceptor: molecular cloning, tissue expression,
            and chromosomal mapping
  JOURNAL   Genomics 41 (3), 360-369 (1997)
  MEDLINE   9731262
REFERENCE   4  (sites)
  AUTHORS   Kubota,R., Kudoh,J., Mashima,Y., Asakawa,S., Minoshima,S.,
            Hejtmancik,J.F., Oguchi,Y. and Shimizu,N.
  TITLE     Genomic organization of the human myocilin gene (MYOC) responsible
            for primary open angle glaucoma (GLC1A)
  JOURNAL   Biochem. Biophys. Res. Commun. 242 (2), 396-400 (1998)
  MEDLINE   9813364
REFERENCE   5  (bases 1 to 1228)
  AUTHORS   Shimizu,N. and Kudoh,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-1997) to the DDBJ/EMBL/GenBank databases.
            Nobuyoshi Shimizu, Keio University School of Medicine, Department
            of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582,
            Japan (E-mail:shimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370(ex.2720), Fax:81-3-3351-2370)
FEATURES             Location/Qualifiers
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Best Local Similarity   99.4%;  Pred. No. 5e-258;
Matches 1217;  Conservative   0;  Mismatches   1;  Indels   6;  Gaps  2;
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Db    1 GATCTCCAGTTCCTAGCATAGTGCCTGGCCACAGTCAGTTCTCAATGAGTTTGCAGAGT 60

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Db  121 GTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTAAAAACCAGGTGGGAGATAT 178

Qy 5042 aggaactattattgggtatggggtgtcataaattgggatgtctcttttttaaaagaaactcc 5101
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Db  179 AGGAACTATTATTGGGTATGGGGTGTCATAAATTGGGATGTCTCTTTTTTAAAAGAAACTCC 238

Qy 5102 aaacagaacttctggaaggttattttctaagaaatcttgctggcagcgtgaaggcaacccc 5161
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Qy 5162 ctgtgcagcgccccaccacccagccctcacgtggccaccctgtcctccccatgaaggggctgg 5221
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Qy 5282 aggcaccctctcaagcacagagagcttcccaggaggaagctccacaagcctctgcaatgag 5341
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Qy 5342 gttctctctgtgcacgttgctcgacagctttgggatggccagctgtccagctgtgctgct 5401
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Db  479 GTTCTCTCTGTGCACGTTGCTCGACAGCTTTGGGCCTGTTTGGGATGGCCAGCTGTCCAGCTGTGCT 538

Qy 5402 tctggcctgcctggttgtggaggtgggggccaggacaagctcagctcaggaggaggccaatga 5461
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Db  539 TCTGGCCTGCCTGGTTGTGGGGGTGGGGGCCAGGACAAGCTCAGCTCAGGAGGAGGCCAATGA 598

Qy 5462 ccagagtgtggccagtatacctttcagtgtgtcccaatgaatccaggtgcc 5521
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Qy 5522 agagcagagccaggccatgtcagtcatccataactttacagagagagacacagccaccaacg 5581
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Qy 5582 cttagacctggaggcccacccaccaaagctcgaccccctcccctggagagaagccctcccaatt 5641
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Db  779 GACCTTGGACCAGGCTGCCAGGCCCCAGGCCCAGGCAGAGAGGGGCTGCAGGAGGGGAGCTGGG 838

Qy 5702 caccctgaggcgggagcggggaccaggctgggaaaccaaaccagagagagttgagaactgccta 5761
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Db  779 GACCCTGAGGCGGGAGCGGGGACCAGGCTGGGAAACCCAAACCAGAGAGAGTTGGAGAACTGCCTA 5761
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RESULT 6
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DEFINITION  Homo sapiens GLC1A (trabecular meshwork induced glucocorticoid
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ACCESSION   Z97171
VERSION     Z97171.1  GI:2425156
KEYWORDS    GLC1A.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1086)
  AUTHORS   Stone,E.M., Fingert,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R.,
            Sunden,S.L., Nishimura,D., Clark,A.F., Nystuen,A., Nichols,B.E.,
            Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C.
  TITLE     Identification of a gene that causes primary open angle glaucoma
  JOURNAL   Science 275 (5300), 668-670 (1997)
  MEDLINE   97158493
REFERENCE   2  (bases 1 to 1086)
  AUTHORS   Adam,M.F., Belmouden,A., Binisti,P., Brezin,A.P., Valtot,F.,
            Bechetoille,A., Dascotte,J.C., Copin,B., Gomez,L., Chaventre,A.,
            Bach,J.F. and Garchon,H.J.
  TITLE     Recurrent mutations in a single exon encoding the evolutionarily
            conserved olfactomedin-homology domain of TIGR in familial
            open-angle glaucoma
  JOURNAL   Hum. Mol. Genet. 6 (12), 2091-2097 (1997)
  MEDLINE   97472461
REFERENCE   3  (bases 1 to 1086)
  AUTHORS   Garchon,H.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-1997) Garchon H.-J., Hopital Necker, INSERM U25,
            161 rue de Sevres 75743 Paris cedex 15 FRANCE
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ORIGIN
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Left column sequence alignment (Db / Qy):

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Qy  5822  aaatgtagaatctggccagggaggcgttgggaaagcagcagcagtcttgggaagggctgagaag  5881
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Db   959  AAATGAGAATCTGGCCACGGAGGTTTGGGAAAGCAGCAGCAGTCAGGAGGGTAGCAAGGCTGAGAAG  1018
Qy  5882  gggccagtgtccccagacgcgagacacgtgtgtccacccaggcctcagagaag         5941
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Db  1019  GGGCCACTGTGTCCCAGACGCGAGACACGTGTGTGCCACCCAGGCCTCCAGAAGG       1078
Qy  5942  taagaatgcagagtgggggactcagaagttcagcagtgatatgtggcctagtgacctgc    6001
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Db  1079  TAAGAATGCAGAGTGGGGGACTCTGAAGTTCAGCAGGTGATATGGCTCGTAGTGACCTGC  1138
Qy  6002  tacaggcggctccaggcctc----------cctgccccttcctcctagagactgcacagctagcacaca   6057
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Db  1139  TACAGGCGGCTCCAGGCCTCCCTGCCCCTTTCCTCCTAGAGACTGCACAGCTAGCACACA  1198
Qy  6058  gacagatgaattaaggaaagcaca  6081
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Right column:

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Query Match     17.6%;  Score 1084.4;  DB 93;  Length 1086;
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Matches 1085;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

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Db     1  AGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTGCAGAGTGAATGGAAATATAA    60
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Db   361  TAAACCTCTCTGAGCTCGGGCATGAGCGCCAAGGCCACCATCCAGGCACCTCTCAGC   420
Qy  5296  acagcagagcttccaggaggagcctcaccaaggcctctgcaatgaggttcttctgtgtcac  5355
          ||||||||||||||||||||||||||||||||||||||
Db   421  ACAGCAGAGCTTCCAGGAGGAGCCTCACCAAGGCCTCTGCAATGAGGTTCTTCTGTGTCAC   480
Qy  5356  gttgctgcagcttggggctgaagatgcagctgtccagctgctgctcctggcctctgctgg  5415
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Db   481  GTTGCTGCAGCTTTGGGCCTGAGATGCCAGCTGTCCACCTGCTGCTTCTTGGCCTGCTGG   540
Qy  5416  tgtgggatgtggggccaggacagctcagctaggaggacacagagagtggccgat  5475
          |||||||||||||||||||||||||||||||||||||||
Db   541  TGTGGGATGTGGGGCCAGGACAGCTCAGCTAGGAGGAGCCAATGACCAGGAGCCGAT   600
Qy  5476  gccagtatacttcagtgtggccagtcccaatgaatccagctgccagagagcagagccagg  5535
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RESULT  7

LOCUS       D88214      1934 bp      mRNA      PRI      07-FEB-1999
DEFINITION  Homo sapiens mRNA for myocilin, complete cds.
ACCESSION   D88214
VERSION     D88214.1  GI:2627176
KEYWORDS    myocilin.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1934)
  AUTHORS   Shimizu,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.
            Nobuyoshi Shimizu, Keio University School of Medicine, Department
            of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160,
            Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-2370,
            Fax:03-3351-2370)
REFERENCE   2  (sites)
  AUTHORS   Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
            Mashima,Y., Oguchi,Y. and Shimizu,N.
  TITLE     A novel myosin-like protein (myocilin) expressed in the connecting
            cilium of the photoreceptor: molecular cloning, tissue expression,
            and chromosomal mapping
  JOURNAL   Genomics 41 (3), 360-369 (1997)
  MEDLINE   97312692
COMMENT     On Nov 20, 1997 this sequence version replaced gi:2104213.
            Sequence updated (17-Nov-1997).
FEATURES             Location/Qualifiers
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     CDS             65..1579
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                     GRCQYTFSVASPNESSCPEQSQAMSVIHNLQRDSSTQRLDLEATKARLSSLESLLHQL
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                     QENENLARRLESSSQEVARLRGQCPRDTARAVAVPPGSREVSTWNLDTLAFQEIKSE
                     LTEVPASRILKESPSGYLRSGEGDTGCGELVWVGEPLTLRAETTIGKYGVWMRDKP
                     TYPYTQDTTWRIDTVGTDVRQVFEYDLISQMQGPSKVHILPRPLESTGAVVYSGSL
                     YFQGAESRTYTRYELNTETVAAEKEIPGAGYHGQFPYSWGGYTDIDLAVEBAGLWVIY
                     STDEAKGAIVLSKLNPENLELEQTWETNIRKQSVANAFIICGTLYTVSSYTSADATVN
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     misc_feature    413..562
                     /note="leucine zipper-like motif 2"
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     polyA_signal    1928..1933
BASE COUNT      510 a      503 c      525 g      396 t
ORIGIN
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Query Match      10.6%;  Score 651.2;  DB 91;  Length 1934;
Best Local Similarity   99.5%;  Pred. No. 1.7e-136;
Matches  653;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy   5287  cctccaagacacagcagagcttcccagagaggaaagcctcaccaaagcctctgcaatgaggtct  5346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     15  cCGGCTCTGCACACAGCAGAGCTTTCCAGAGGAAGCCCTCACCAAGCCTCTGCAATGAGGTTCT    74

Qy   5347  tctgtgcacgttgtctcagtcttttgggcctgaagtgcagctgtccagctgctgtctctctg  5406
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Db     75  TCTGTGCACGTTGCTGCAGCTTTTTGGGCCTGAGATGCCAGCTGTCCAGCTGCTGCTTCTG   134

Qy   5407  cctgcctggttgtgtgggatgtgggggccaggacagctaggtccaggaaggaggccaatgaccaga  5466
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Db    135  CCTGCCTCGGTGTGTGGGATGTGGGGGCCAGGACAGCTCAGGAAGGCCAATGACCAGA   194

Qy   5467  gtggccgatgccagtataccttcagtgtgtgccagtcccaatgaatccagctgcccagagc  5526
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Db    195  GTGGCCCGATGCCAGTATACCTTCAGTGTGTGCCAGTCCCAATGAATCCAGCTGCCCAGAGC   254

Qy   5527  agagcaaggccatgtcagtcatcccaaccttaccagagacagcagcacaacgcttag  5586
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255  AGAGCCACAGGCCATGTCAGTCATCCATAACTTACAGAGACAGCAGCACAACGCTTAG   314

Qy   5587  acctggaggccaccaaagctcgactcagctccctgggaagctcctccaccaattgacct  5646
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315  ACCTGGAGGCCACCAAAGCTCGACTCAGCTCCCTGGGAAGCTCCTCCACCAAGCTGACCT   374

Qy   5647  tggaccaaggctgccaggccccagggagagaccaggagaggggctggcaggacacc  5706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375  TGGACCAAGGCTGCCAGGCCCCAGGAGGAGACCAGGAGAGGGGCTGGGCAGGCACCC   434

Qy   5707  tgaggcgggagcgggagaccagctggaaacccagagaggttgggagctgcctacagca  5766
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Db    435  TCAGGCGGGAGCGGGACCAGCTGGAAACCCAAACCAGAGAGGTTGGAGACTGCTACCA   494

Qy   5767  acctcctccgagacaagtcagttctgaggagaagaagaagaagcgactaaggacaagaaaatg  5826
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495  ACCTCCTCCGAGACAAGTCAGTTCTGGAGGAGGAGAAGAAGCGGCTAAGGCAAGAGAATG   554

Qy   5827  agaatctggccaggaggttggaaagcagcagggtaggaaggctggaggggcc  5886
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Db    555  AGAATCTGGCCAGGAGGTTGGAAAGCAGCAGGGTAGGAAGGCTGGAGGGGCC   614

Qy   5887  agtgtccccagacccgagacactgctcgggtctgtgcaccaggctccagagagaaggt  5942
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Db    601  GCCAGTATACCTTCAGTGTGTGCCAGTCCCAATGAATCCAGCAGCAGAGCCAG    660
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Qy   5536  ccatgtcagtcatcccaataacttacagagacagcagcacacaacgcttagacctggagg    5595

Db    661  CCATGTCAGTCATCCATAACTTACACAGAGACAGCAGCACAACGCTTAGACCTGGAGG    720
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Qy   5596  ccaccaaagctcgactcagctccctgggagagctcctccaccaattgacctggaccagg    5655

Db    721  CCACCAAAGCTCGACTCACCTCCCTGGGAGAGCCCTCCTCCACCAATTGACCTTGACCAGG    780
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Qy   5656  ctgccaggcccagggagagaccaggagagggggctgggacacctgaggcggg    5715

Db    781  CTGGCCAGGCCCCAGGAGGAGACCAGGAGAGGGGCTGGGCACCTGAGGCGGG    840
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Qy   5716  agcgggaccagctggaaacccagaagttgggagactgcctacagacctcctcc    5775

Db    841  AGCGGGACCAGCTGGAAACCCAAACCAGAGAGGTTGGAGACTGCTACAGAAACCTCCTCC    900
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Qy   5776  gagacaagtcagttctggaggagaagaagaacgactaaggcaagaatctgg    5835

Db    901  GAGACAAGTCAGTTCTGGAGGAGAAGAAGCGACTAAGGCAAGAAAATGAGAAATCTGG    960
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Qy   5836  ccaggaggttggaaagcagcagggtagcaaggcctggaggggccagtgtgtcccc    5895

Db    961  CCAGGAGGTTGGAAAGCAGCAGGGTAGCAAGGGGCTAGCAGGGGCCAGTGTCCCC    1020
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Qy   5896  agacccgagacactgctcggggtctgtgcaccaggctccagagagaaaggctaag    5955

Db   1021  AGACCCGAGACACTGCTCGGGGTCTGTGCCACCAGCCTCCAGAGAGAAGGTAACAAATGCAGAGT    1080
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Qy   5956  ggggg 5961

Db   1081  GGGGG 1086
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RESULT   8

Db    AX004457

LOCUS       AX004457     1871 bp   DNA      PAT   24-AUG-2000
DEFINITION  Sequence 1 from Patent WO9916898.
ACCESSION   AX004457
VERSION     AX004457.1  GI:9927916
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1871)
  AUTHORS   Anctil,J.L. and Cote,G.
  TITLE     Molecular diagnostic of glaucomas associated with chromosomes 1,
            and method of treatment thereof
  JOURNAL   Patent: WO 9916898-A 1 08-APR-1999;
            ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)
FEATURES             Location/Qualifiers
     source          1..1871
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      499 a    483 c    507 g    382 t
ORIGIN

Query Match             10.4%;  Score 640.4;  DB 9;  Length 1871;
Best Local Similarity   99.8%;            Pred. No. 4.5e-134;
Matches  641;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    5301 agagcttccagagaggaagcctcaccaagcctctgcaatgtaggtctgttctcttgcacgttgc 5360
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Db       1 agagcttccagagaggaagcctcaccaagcctctgcaatgtaggtctgttctcttgcacgttgc 60

Qy    5361 tgcagcttgggcctgagatgcagctgtctgctgctgggctgcgtgtgg 5420
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Db      61 tgcagcttgggcctgagatgcagctgtctgctgctgggctgcgtgtgg 120

Qy    5421 gatgtgggggccaggacagctcagtcaaggaaggccaatgaccaagtggccgatgccag 5480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gatgtgggggccaggacagctcagtcaaggaaggccaatgaccaagtggccgatgccag 180

Qy    5481 tataccttcagtgtgtggccagtcccaatgaatccagctgcccagagcagagccaggccatg 5540
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Db     181 TATACCTTCAGTGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGCCAGGCCATG 240

Qy    5541 tcagtcatccataacttacagagagacagcacccaacgcttagacctggaggccacc 5600
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Db     241 TCAGTCATCCATAACTTACAGAGAGACAGCACCCAACGCTTAGACCTGGAGGCCACC 300

Qy    5601 aaagctcgactcagctccctggagagctgcc 5660
           |||||||||||||||||||||||||||||||
Db     301 AAAGCTCGACTCAGCTCCCTGGAGAGCTGCC 360

Qy    5661 aggccccaggagaccccaggagggggctgggcacccctgagcgggaacgg 5720
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Db     361 AGGCCCCAGGAGACCCCAGGAGGGGGCTGGGCACCCCTGAGCGGGAACGG 420

Qy    5721 gaccagctggaaacccaaaccacagagagttggagactgcctacagacgaacctcctccgac 5780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GACCAGCTGGAAACCCAAACCACAGAGAGTTGGAGACTGCCTACAGACGAACCTCCTCCGAC 480

Qy    5781 aagtcagtcttctgagaganagcagagcgactaaggcagagaaaatcagaaactctggccacg 5840
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Db     481 AAGTCAGTTCTGAGAGANAGCAGAGCGACTAAGGCAGAGAAAATCAGAAACTCTGGCCAGG 540

Qy    5841 aggttggaaaagcaacagcceaggaaggtagcaaggctggagaaggggccagtgtcccagacc 5900
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Db     541 AGGTTGGAAAAGCAGCAGCAGGAGGTGAGAAAGGGCCAGTGTCCCAGACC 600

Qy    5901 cgagacaactgctctgggctgtgccaccaggtccagagaggaggt 5942
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Db     601 CGAGACACTGCTCTCGGGCTGTGCCACCAGGCTCCAGAGAGAGT 642
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RESULT   9

Db    AX004474

LOCUS       AX004474     1871 bp   DNA      PAT   24-AUG-2000
DEFINITION  Sequence 18 from Patent WO9916898.
ACCESSION   AX004474
VERSION     AX004474.1  GI:9927933
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1871)
  AUTHORS   Anctil,J.L. and Cote,G.
  TITLE     Molecular diagnostic of glaucomas associated with chromosomes 1,
            and method of treatment thereof
  JOURNAL   Patent: WO 9916898-A 18 08-APR-1999;
            ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)
FEATURES             Location/Qualifiers
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                     /protein_id="CAC04896.1"
                     /db_xref="GI:9927934"
                     /translation="MRFPCARCCSFGPEMPAVQLLLLACLVWDVGARTAQLRKANDQS
                     GRCRQYTFSVASPNESSCPEQSQAMSVIHNLQRDSSTORLDLEATKARLSSLESLLHQL
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                     QENRLARRLESSSQEVARLRRCQCPQTRDTARAVPPGSREVSTWNLDTLAFOELKSE
                     LTEVPASRILKESPSGYLRSGEGDTGCGELVWWGEPLTLRTAETIITGKYGVWMRDPKP
                     TYPYTQETTWRIDTVGTDVRQVEYDLLSQFMQGYPSKVHILPRPLESTGAVVYSGSL
                     YFQGAESRVIVRELNTETVKAEKEIPCAGYHQOFPYSWGGYTDIDLAVDEAGLWVIY
                     STDEAKGAIVLSKLNPENLELEQTWETINIRKQSVANAFIICGTLYTVSSYTSADATVN
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BASE COUNT      499 a    483 c    507 g    382 t
ORIGIN

Query Match             10.4%;  Score 640.4;  DB 9;  Length 1871;
Best Local Similarity   99.8%;            Pred. No. 4.5e-134;
Matches  641;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    5301 agagcttccagagaggaagcctcaccaagcctctgcaatgtaggtctgttctcttgcacgttgc 5360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    5361 tgcagcttgggcctgagatgcagctgtctgctgctgggctgcgtgtgg 5420
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCAGCTTTGGGCCTGAGATGCAGCTGTCTGCTGCTGGGCTGCGTGTGG 120

Qy    5421 gatgtgggggccaggacagctcagtcaaggaaggccaatgaccaagtggccgatgccag 5480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GATGTGGGGGCCAGGACAGCTCAGTCAAGGAAGGCCAATGACCAAGTGGCCGATGCCAG 180

Qy    5481 tataccttcagtgtgtggccagtcccaatgaatccagctgcccagagcagagccaggccatg 5540
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Qy    5541 tcagtcatccataacttacagagagacagcacccaacgcttagacctggaggccacc 5600
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Qy    5601 aaagctcgactcagctccctggagagctgcc 5660
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Qy    5661 aggccccaggagaccccaggagggggctgggcacccctgagcgggaacgg 5720
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RESULT 10
LOCUS       AR030962
DEFINITION  Sequence 2 from patent US 5861497.
ACCESSION   AR030962
VERSION     AR030962.1  GI:5944176
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1999)
  AUTHORS   Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE     Trabecular meshwork induced glucocorticoid response (TIGR) nucleic
            acid molecules
  JOURNAL   Patent: US 5861497-A 2 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1..1999
                     /organism="unknown"
BASE COUNT     537 a    508 c    534 g    420 t
ORIGIN

LOCUS       AR030962      1999 bp    DNA                 PAT        29-SEP-1999

Query Match        10.4%;  Score 640.4;  DB 9;  Length 1999;
Best Local Similarity 99.8%;  Pred. No. 4.5e-134;
Matches  641;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  5301 agagctttccagaggaaggcctccaccaagcctctgcaatgagtcttctctgtgacgttgc 5360
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Db     1 AGAGCTTTCCAGAGGAAGGCCTCCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy  5361 tgcagcttggggtcagctgtgccagctgctctggcctggtgtgtgtg 5420
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Db    61 TGCAGCTTTGGGGTCTGAGATGCCAGCTGTCTCCAGCTGGTGTGTGTGG 120

Qy  5421 gatgtgggggccaggacagctcagctcagggaaggccaatgaacagagagtggccgatgccag 5480
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Db   121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy  5481 tatacccttcagtgtggccagtcccaatgaatccagctgcccagagccagaggccatg 5540
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Qy  5541 tcagtcataacttacagagagacagcagcacccaaccgcttagacctggaggccacc 5600
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Db   241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACCGCTTAGACCTGGAGGCCACC 300

Qy  5601 aaagctcgactcagctccctggagagccctcctccaccagcacccagagggcgggaacgg 5660
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Db   301 AAAGCTCGACTCAGCTCCCTGGAGAGCCTCCTCCACCAGCACCCAGAGGGCGGGGAACGG 360

Qy  5661 aggcccagaggagaacccaggaaggggctgcagagagggggagctgggcaccctgaggcggaggccgg 5720
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Qy  5721 gaccagctggaaacccaaaccagagagtcggagactgtcctacgcagccaaccctcctccgagac 5780
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Db   421 GACCAGCTGGAAACCCAAACCAGAGAGTTGGAGACTGCCTACGCAGCCAACCCTCCTCCGAGAC 480

Qy  5781 aagtcagttctggaggaggaagagcgactaaggcaagaataaatcagcaacctcctccagagac 5840
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Qy  5841 aggttggaaagcagcagccagcagccagtgtcccagacc 5900
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Db   541 AGGTTGGAAAGCAGCAGCCAGTGTCAGAGAGGGGCCAGTGTCCCCAGAC 600

Qy  5901 cgagacactgctcggggctgtgccacccaggcttccagagagaagtt 5942
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Db   601 CGAGACACTGCTCGGGGCTGTGCCACCCAGGCTCCCAGAGAAGTT 642
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RESULT 11
LOCUS       AR066022
DEFINITION  Sequence 2 from patent US 5849879.
ACCESSION   AR066022
VERSION     AR066022.1  GI:5996238
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1999)
  AUTHORS   Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE     Methods for the diagnosis of glaucoma
  JOURNAL   Patent: US 5849879-A 2 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1..1999
                     /organism="unknown"
BASE COUNT     537 a    508 c    534 g    420 t
ORIGIN

LOCUS       AR066022      1999 bp    DNA                 PAT        29-SEP-1999

Query Match        10.4%;  Score 640.4;  DB 9;  Length 1999;
Best Local Similarity 99.8%;  Pred. No. 4.5e-134;
Matches  641;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  5301 agagctttccagaggaaggcctccaccaagcctctgcaatgagtcttctctgtgacgttgc 5360
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Db     1 AGAGCTTTCCAGAGGAAGGCCTCCACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60

Qy  5361 tgcagcttggggtcagctgtgccagctgctctggcctggtgtgtgtg 5420
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Db    61 TGCAGCTTTGGGGTCTGAGATGCCAGCTGTCTCCAGCTGGTGTGTGTGG 120

Qy  5421 gatgtgggggccaggacagctcagctcagggaaggccaatgaacagagagtggccgatgccag 5480
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Db   121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy  5481 tataccttcagtgtggccagtccaatgaatccagctgcccagagccagaggccatg 5540
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Db   181 TATACCTTTCAGTGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGGCCATG 240

Qy  5541 tcagtcataacttacagagagacagcagcacccaaccgcttagacctggaggccacc 5600
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Db   241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACCGCTTAGACCTGGAGGCCACC 300

Qy  5601 aaagctcgactcagctccctggagagccctcctccaccagcacccagagggcgggaacgg 5660
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Db   301 AAAGCTCGACTCAGCTCCCTGGAGAGCCTCCTCCACCAGCACCCAGAGGGCGGGGAACGG 360

Qy  5661 aggcccagaggagaacccaggaaggggctgcagagagggggagctgggcaccctgaggcggaggccgg 5720
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Qy  5721 gaccagctggaaacccaaaccagagagtcggagactgtcctacgcagccaaccctcctccgagac 5780
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Db   481  AAGTTCAGTTCTGGGAAGAAAGAAGAAGAGAGAAGAAGAGAAAATGAGAAATCTGGCCAGG 540
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Db   541  AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGCTGAGGAAAGGGGCCAGTGTCCCAGACC 600
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Qy  5901  cgagacactgctcgggcgtgtgccaccaggctccagagagaaggt 5942

Db   601  CGAGACACTGCTCGGGCGTGTGCCACCAGGCTCCAGAGAAGTT 642
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RESULT 12
LOCUS          AR069089                    1999 bp    DNA        PAT   29-SEP-1999
DEFINITION     Sequence 2 from patent US 5854415.
ACCESSION      AR069089
VERSION        AR069089.1  GI:6001296
KEYWORDS
SOURCE         Unknown.
  ORGANISM     Unknown.
               Unclassified.
REFERENCE      1  (bases 1 to 1999)
  AUTHORS      Nguyen,T.D., Polansky,J.R. and Huang,W.
  TITLE        Methods for the diagnosis of glaucoma
  JOURNAL      Patent: US 5854415-A 29-DEC-1998;
FEATURES             Location/Qualifiers
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BASE COUNT      537 a     508 c     534 g     420 t
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Query Match    10.4%;  Score 640.4;  DB 9;  Length 1999;
Best Local Similarity  99.8%;
Matches  641;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
            Pred. No. 4.5e-134;
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Db     1  AGAGCTTTCCAGAGGAAGCCTCACCAAGCCTCTGCAATGAGGTTCTTCTCTGTCACGTTGC 60

Qy  5361  tgcagctttgggcctgagatccaggccagctgtccagctgtctctgtgttcttgtgtgg 5420
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Db   121  GATGTGGGGCCAGGACAAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180

Qy  5481  tatacttcagtgtggccagtcccaatgaatccagctgtccagagagacagagccaggccatg 5540
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Db   181  TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGTCCAGAGAGACAGAGCCAGGCCATG 240

Qy  5541  tcagtcaatccataacttacagagagacacccaaacgcttagacctggaggccaacc 5600
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Db   301  AAAGCTCGACTCAGCTCCCTGGAGAGCCTCTCCACCAAATTGACCTTGGACCAGGCTGCC 360

Qy  5661  agggcccagagaacccagggggtcagaggagtgtggcaccctgagggggaggcgg 5720
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Qy  5781  aagtcagttctgggaggaagaagcgcgactaagcacagaaatgagaatctgtgccagg 5840
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DEFINITION     Human trabecular meshwork inducible glucocorticoid response protein
               (TIGR) mRNA, complete cds.
ACCESSION      U85257
VERSION        U85257.1  GI:2978428
KEYWORDS
SOURCE         human.
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 2000)
  AUTHORS      Nguyen,T.D. and Polansky,J.R.
  TITLE        Glucocorticoid effects on HTM cells: Molecular Biology Approaches
  JOURNAL      Glaucoma Update 4, 331-343 (1991)
REFERENCE      2  (bases 1 to 2000)
  AUTHORS      Stone,E.M., Fingert,J.H., Alward,W.L.M., Nguyen,T.D.,
               Polansky,J.R., Sunden,S.L.F., Nishimura,D., Clark,A.F., Nystuen,A.,
               Nichols,B.E., Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and
               Sheffield,V.C.
  TITLE        Identification of a gene that causes primary open angle glaucoma
  JOURNAL      Science 275 (5300), 668-670 (1997)
  MEDLINE      97158493
REFERENCE      3  (bases 1 to 2000)
  AUTHORS      Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
               Polansky,J.R.
  TITLE        Gene structure and properties of TIGR, an olfactomedin-related
               glycoprotein cloned from glucocorticoid-induced trabecular meshwork
               cells
  JOURNAL      J. Biol. Chem. 273 (11), 6341-6350 (1998)
  MEDLINE      98165818
REFERENCE      4  (bases 1 to 2000)
  AUTHORS      Nguyen,T.D. and Polansky,J.R.
  TITLE        Direct Submission
  JOURNAL      Submitted (13-JAN-1997) Ophthalmology, University of California San
               Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
REFERENCE      5  (bases 1 to 2000)
  AUTHORS      Nguyen,T.D.
  TITLE        Direct Submission
  JOURNAL      Submitted (02-APR-1997) Ophthalmology, University of California San
               Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
REFERENCE      6  (bases 1 to 2000)
  AUTHORS      Nguyen,T.D.
  TITLE        Direct Submission
  JOURNAL      Submitted (19-MAR-1998) Ophthalmology, University of California San
               Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA
  REMARK       Sequence update by submitter
COMMENT        On Mar 19, 1998 this sequence version replaced gi:1945067.
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Qy  5841  aggttggaaagcagcagccaggaggtagcaagctgaggaaaggccagtgtcccagacc 5900

Db   541  AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGCTGAGGAAAGGGGCCAGTGTCCCAGACC 600
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Qy  5901  cgagacactgctcgggcgtgtgccaccaggctccagagagaaggt 5942

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       QENLARLESSQEVARLRRQQCPQTRDTARAVPGSREVSTWNLDTLAFQELKSE
       LTEVPASRILKESPSGYLRSGEGDTGCELVWVGEPLTRTAETTITGKYGVWMRDPKP
       TYPYTQETTWRIDTVGTDVDRQVFEYDLISQFMQGYPSKVHILPRPLESTGAVVYSGSL
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3'UTR

BASE COUNT   538 a   508 c   534 g   420 t
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Query Match   10.4%;   Score 640.4;   DB 97;   Length 2000;
Best Local Similarity   99.8%;   Pred. No. 4.5e-134;
Matches   64;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGAGCTTTCCAGAGGAAGCCTCACCAAGCCTCTGCAATGAGGGTTCTTCTCTGTGCACGTTGC 60

Qy   5361 tgcagcttgggcctgagatgccagctgcttctggcctgcctggtgtgg 5420
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Qy   5421 gatgtggggggccaggacaagctcagctcaggaaggccaagctggacagc 5480
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Qy   5481 tataccttcagtgtggccagtcccaatgaatccagcgtcccagagagcaggccatg 5540
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Db   241 TCAGTCATCCATAACTTACAGAGACAGCACCCACACACGCTTAGACCTGGAGGCCACC 300

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Db   301 AAAGCTCGACTCAGCTCCTCCACCAATTGACCTGGACCAGGCTGCC 360

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Db   361 AGGCCCCAGGAGACCCAGGAGGGGCTGCAGAGGAGGAGGACGG 420

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Db   421 GACCAGCTGGAAACCCAAAACCACAGAGTTGGAGACTGCCTACAGCAACCTCCTCCGAGAC 480

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LOCUS   A84847   2002 bp   DNA   PAT   21-JAN-2000
DEFINITION Sequence 2 from Patent WO9844108.
ACCESSION   A84847
VERSION   A84847.1   GI:6733711
KEYWORDS   .
SOURCE   unidentified.
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 2002)
  AUTHORS   Huang,W. and Nguyen,T.D.
  TITLE   DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
  JOURNAL   Patent: WO 9844108-A 2 08-OCT-1998;
            HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES   Location/Qualifiers
     source   1..2002
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BASE COUNT   538 a   508 c   535 g   421 t
ORIGIN

Query Match   10.4%;   Score 640.4;   DB 9;   Length 2002;
Best Local Similarity   99.8%;   Pred. No. 4.5e-134;
Matches   641;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Db   1 AGAGCTTTCCAGAGGAAGCCTCACCAAGCCTCTGCAATGAGGGTTCTTCTCTGTGCACGTTGC 60

Qy   5361 tgcagcttgggcctgagatgccagctgcttctggcctgcctggtgtgg 5420
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Qy   5421 gatgtggggggccaggacaagctcagctcaggaaggccaagctggacagc 5480
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Db   121 GATGTGGGGGCCCAGGACAGCTCAGCTCAGGAAGGCCAAATGACCAGAGTGGCCGATGCCAG 180

Qy   5481 tataccttcagtgtggccagtcccaatgaatccagcgtcccagagagcaggccatg 5540
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Db   181 TATACCTTCAGTGTGTGGCCAGTCCCAATGAATCCAGCGTCCCAGAGAGCAGGCCATG 240

Qy   5541 tcagtcatccataacttacagagacagcacccacacacgcttagaacctggaggccacc 5600
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RESULT 15

LOCUS       A84850                  2000 bp    DNA            PAT       21-JAN-2000
DEFINITION  A84850 Sequence 2 from Patent WO9844107.
ACCESSION   A84850
VERSION     A84850.1  GI:6733713
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2000)
  AUTHORS   Huang,W. and Nguyen,T.D.
  TITLE     DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
  JOURNAL   Patent: WO 9844107-A 2 08-OCT-1998;
            UNIVERISTY OF CALIFORNIA (US); HUANG WEIDONG (US)
FEATURES             Location/Qualifiers
     source          1..2000
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BASE COUNT      538 a    506 c    534 g    422 t
ORIGIN

Query Match             10.3%;  Score 635.6;  DB 9;  Length 2000;
Best Local Similarity   99.4%;           Pred. No. 5.4e-133;
Matches  638;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Qy    5301 agagctttccagagaggaagcctcaccaaagcctctgcaatgtgaggtttcttctgtgcacgttgc 5360
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Db     481 AAGTCAGTTCTGGAGGAAGAAGAGCGACTAAGGCAAGAAAAATGAAGAATCTGGCCAGG 540

Qy    5841 aggttgggaaagcagccaggaggtagcaagggccagtgtcccagagacc 5900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGGTTGGGAAAGCAGCCAGGAGGTAGCAAGGGGCCCAGTGTCCAGTACC 600

Qy    5901 cgagacactgctcgggctgtgccaccaggctccagagaaggt 5942
           |||||||||||||||||||||||||||||||||||||||||||-|
Db     601 CGAGACACTGCTCGGGCTGTGCCACCAGGCTCCAGAGAAGTT 642
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